

Fig. 1

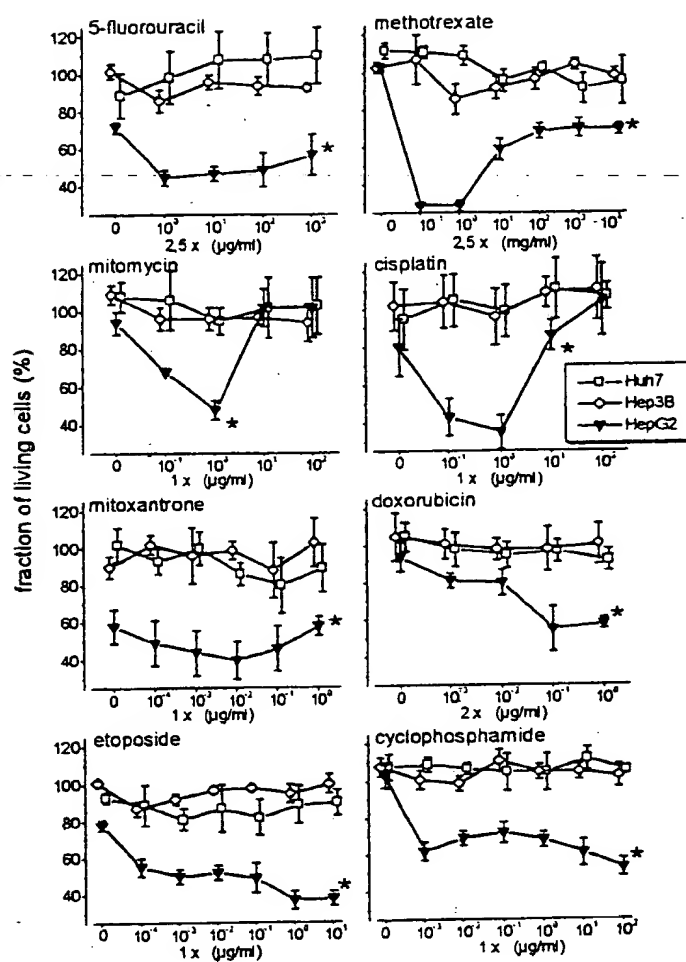


Fig. 2

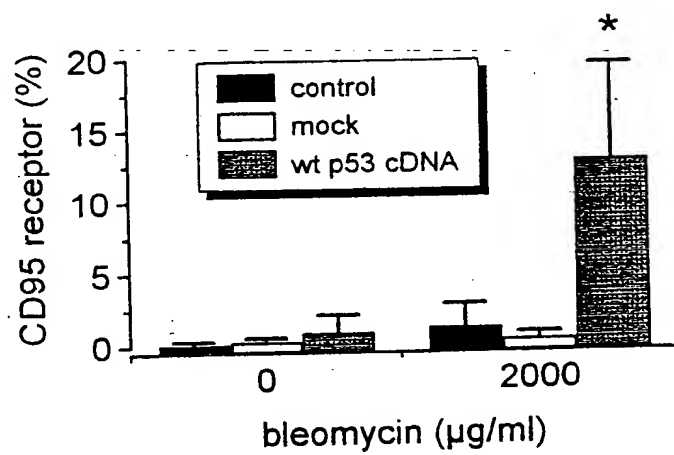


Fig. 3

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620 GATCCCGCTGGGCAGGCGGG 640 GCAGTCCGGCGCTCCTCGG 660 AGACCACTGCGCTCCACGTT  
Sau3A1  
 680 GAGGTGGGCGTGGGGGGCGG 700 ACAGGAATTGAAGCGGAAGT 720 CTGGGAAGCTTTAGGGTCGC  
HindIII  
 740 TGGAGGGGGACCCCGGTTGG 760 AGAGAGGAGCGGAACCTCTG - GACAAGCCCTGACAAGCCAA  
p53BE  
 800 GCCAAAGGTCCGCTCCGGCG 820 CGGGTGGGTGAGTGC CGCGCC 840 GCCCCGCGGGGGCGGGGAGA  
 860 GAGCCTGCAGCCTTCAGAAC 880 AGATAT

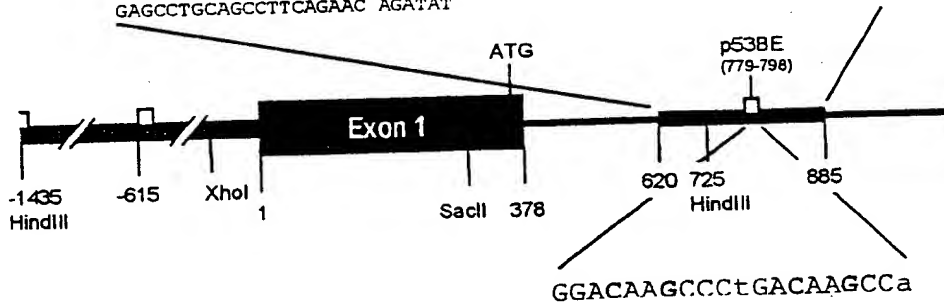


Fig. 4

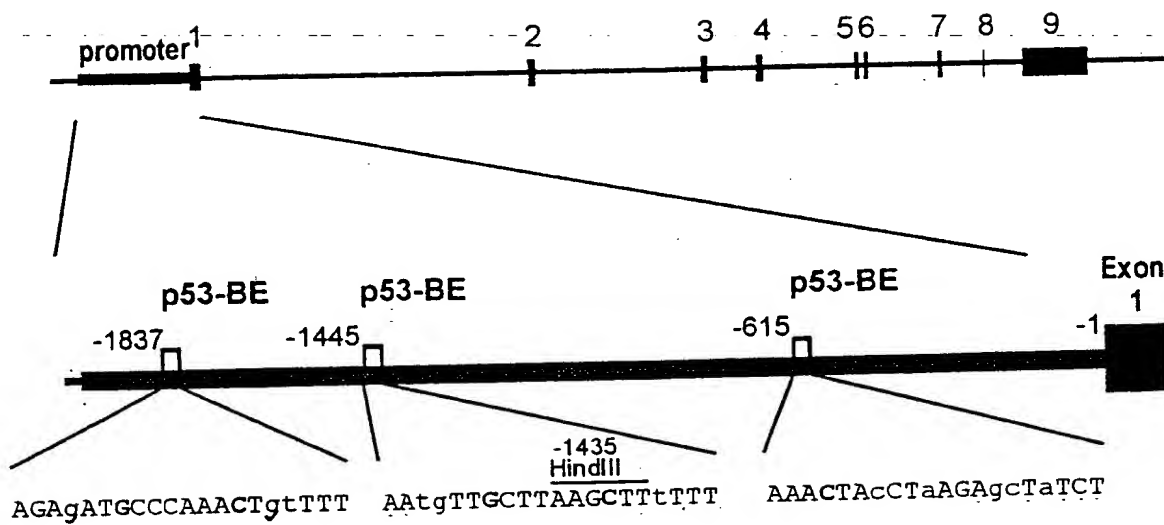


Fig. 5

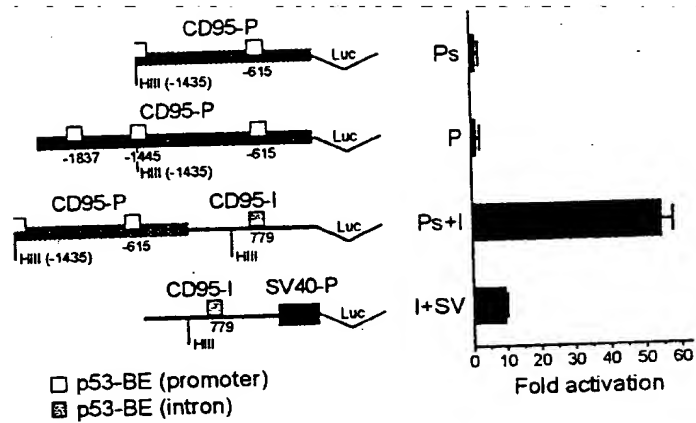


Fig. 6

GATCCCGCTGGGCAGGCGGGGCAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
CTAGGGCGACCCGTCGCCCGTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAA

GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
CTCCACCCGACCCCCCGCCTGTCCTTAACCTTCGCCTTCAGACCCTTCGAAATCCCAGCG

<---- 4. P53-BE ---->  
(intron)

TGGAGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCCTGACAGCCCTGACAGCCAA  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
ACCTCCCCCTGGGGCCAACCTCTCTCCTCGCCTTGAGGACCTGTTCTGGGACTGTTCTGGTT

GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGCGGGGAGA  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
CGGTTTCCAGGCGAGGCCGCGCCCACCACTCACGCGCGGCGGGCGCCCCGCCCTCT

GAGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAA  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
CTCGGATGTCGGAAGTCTTGTGTATAACGAGTAAAGACCGTCAAGAGTCTGCATCCTTT

TAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTT  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
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CTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
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421 -----+-----+-----+-----+-----+-----+-----+ 480  
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AGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTGTGTTTCTGCCCTTCTCTTTCTTTTGG  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
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CCCTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
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TACTCGTTCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGAGCAGCCT  
601 -----+-----+-----+-----+-----+-----+-----+ 660  
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GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGAGATGGCTAATCAAAGAGACGTG  
661 -----+-----+-----+-----+-----+-----+-----+ 720  
CAAACTTTTCAGGGAGCGAGTCTTTACGGTCAACGTCTACCGATTAGTTTCTCTGCAC

TCAGTGTGCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACAT

Fig. 8

2<sup>nd</sup> half of the  
2.p53-BE  
(promoter)

AGCTTTTGGCTACATTTTATTGTAAAG  
448 -----+----- 480  
TCGAAAAACCGATGTAAAAAATAACATTTC

TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC  
481 -----+----- 540  
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTTCATAATTCATTCCTTCTAG

CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT  
541 -----+----- 600  
GTGTATACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA

CCTTTCCCTTTTTTCTCTCTCCCTCCTTCATTCTCTCTCCCTTACCTCTCCTTTC  
601 -----+----- 660  
GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGAATGGAGAGGAAAG

CTTCCCTCACACCCCTTTTCTCTCTCTTTTACATTTTTTTATTAAATGAACTTTTC  
661 -----+----- 720  
GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAAATAAATTTACTTGAAAAG

ATTTTGAATAGTTTTAGGATTTCAAAAAATTGCAGAGATAATACAGAGAATGCCATA  
721 -----+----- 780  
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TACCATCCTCTTATCCCACTTCTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA  
781 -----+----- 840  
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GGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG  
841 -----+----- 900  
CCGACCGTGCGGGTCCCAGAAGGAGTACCGTGATTGTGAGATGACTTTCCACCTTGTCTC

ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG  
901 -----+----- 960  
TGTTGCGATAGTTGTGGATGTTCTGACCACCATTACGTCAGTGTCTACGTTTGTGTCC

GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCCAACAGGCTCCA  
991 -----+----- 1020  
CACTACCTTTCGGGAGTCCTCCCATTTGGATTGGATCTAAACTCCCGGGTTTGTCCGAGGT

GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA  
1021 -----+----- 1080  
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1081 -----+-----+-----+-----+-----+-----+-----+ 1140  
AATTACACAATAATTACCCAACTTAGATTAACCCTTCCCTCTCTCCAACGTCTCACTCCA  
GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA  
1141 -----+-----+-----+-----+-----+-----+-----+ 1200  
CGTCTCGAACCACCTGCTACGGTTTCCTTATGACTTTGGAAATCACACAGGTCAGACCTT  
CTGCATCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATACTTCTGTAAAATT  
1201 -----+-----+-----+-----+-----+-----+-----+ 1260  
GACGTAGGTTTAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

←--- 3.p53-DE ----→  
(promoter)

CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT  
 1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320  
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 TCACCAGAGCACGAAAGAATTACAAGATTTTTTTTTTAAAGAAAATTGGCCAGGAAATAAT  
 1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380  
 AGTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCTTTTATTA  
 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGGGGCTATGCGATTTG  
 1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440  
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 1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500  
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 1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560  
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 GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCAGTCAAATGCCCGCAAG  
 1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620  
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 GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAATTCCCAGGTTGAACTACAGCAGAA  
 1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740  
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 GCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGC  
 1741 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1800  
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 CACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTGCAACGAACCTGACTCCTTCC  
 1801 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1860  
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 TCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC  
 1861 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1920  
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[illegible]

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 1980 GGAGGGGTTGGGCCCGCAAGGGTTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG  
 1981 TTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT  
 2040 AAAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCCACAAGTTTCTGCGAA  
 2041 CTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTG  
 2100 GACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCGTGAC  
 2101 GCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCCCGC  
 2160 CGTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCG  
 2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTTA  
 2220 CCTGTACATGTCTCGAGCTCTTCATGATCACCAGGTGCACCCGGCACGTGGAATTCGAAT  
 ←---4.p53-BE-  
 (intron)  
 2221 GGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCCTGGACAAGCCCTGAC  
 2280 CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCCTCGCCTTGAGGACCTGTTCCGGGACTG  
 ----->  
 2281 AAGCCAAGCCAAAGSTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGC  
 2340 TTCGGTTCGGTTTTCCAGGCGAGGCCGCGCCACCCACTCAGCGCGGCGGGGCGCCCCG  
 2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTTCTCAGACG  
 2400 CCCCTCTCTCGGACGTCGGAAGTCTTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC  
 2401 TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAAGGCACCT  
 2460 ATCCTTTATTTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGA  
 2461 TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT  
 2520 AAAGAAAGAGCTTTTTCAATATAACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA  
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 2580 AAAATAACAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAAT  
 2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTTTTGTCTTCTGCCCTTCTCTTTCT  
 2640 CTGACATTACGCGACGGACTACCAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA  
 2641 TCTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGG  
 2700 AGAAAACGGGAAAGAATCGAACGTGAGGGTACCATAAAGACGAACAGAGGACGACCCC

T02TH0-TEHE000

2701 TTGGTGGTACTCGTTCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA  
-----+-----+-----+-----+-----+ 2760  
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2761 GCAGCCTGTTTTGAAAAATCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG  
-----+-----+-----+-----+ 2820  
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2821 AGACGTG  
----- 2827  
TCTGCAC

T02F40-T624E860

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Fig. 9

<---- 1.p53-BE ---->

1 TGAGGACTCTCAGGAATATGCTGGTAAAATAAAAATAACCTTTAGAGATGCCCAAACCTGT  
-----+-----+-----+-----+-----+-----+ 60  
ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAAATCTCTACGGGTTTGACA  
-->  
61 TTTCCCCAGAACACCAGCATTATTAGGTGTTTCAATAGATTCTTCAAAGGATTCCA  
-----+-----+-----+-----+-----+-----+ 120  
AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCCTAAGGT  
AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCTTTGACATTAGCATAC  
121 -----+-----+-----+-----+-----+-----+ 180  
TTCCGTTTCTTCAAACCCCTTGTCATATATATTAATGGGTTGGGAACTGTAATCGTATG  
TAAGGGCCCTGAGAAGTTTGGATTAAGAAAGTTTCAAATTAAAGTAACCCAGAATTTT  
181 -----+-----+-----+-----+-----+-----+ 240  
ATTCCCGGACTCTTCAAACCTAATTCTTTCAAAGTTTAATTTATTGGGTCTTAAAA  
CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT  
241 -----+-----+-----+-----+-----+-----+ 300  
GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA  
GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGGTATGGCATAGA  
301 -----+-----+-----+-----+-----+-----+ 360  
CTTGAACCTCTATTAATCTGCATGCACCCATCTCCCATCCCCTCCCCCATACCGTATCT  
AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA  
361 -----+-----+-----+-----+-----+-----+ 420  
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<---- 2.p53-BE ---->

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-----+-----+-----+-----+-----+-----+ 480  
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481 -----+-----+-----+-----+-----+-----+ 540  
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541 -----+-----+-----+-----+-----+-----+ 600  
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CCTTTCCCCTTTTTTCTCTCTTCCCTCCTTCATTCCTTCTTCCCTTACCTCTCCTTTT  
601 -----+-----+-----+-----+-----+-----+ 660  
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008429-0440

661 CTTCCCTCACACCCCTTTTCCTTCCTTCTTTTTACATTTTTTTTATTTAAATGAACCTTTTC 720  
 -----+-----+-----+-----+-----+-----+-----+  
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 721 ATTTTGGAAATAGTTTTAGGATTTCAAAAAATTGCAAGAGATAATACAGAGAATGCCATA 780  
 -----+-----+-----+-----+-----+-----+-----+  
 TAAACCTTATCAAAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT  
 781 TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA 840  
 -----+-----+-----+-----+-----+-----+-----+  
 ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT  
 841 GGCTGGCACGCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG 900  
 -----+-----+-----+-----+-----+-----+-----+  
 CCGACCGTGCGGGTCCCAGAAGGAGTACCGTGATTGTCAGATGACTTTCCACCTTGTCTC  
 901 ACAAGGCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG 960  
 -----+-----+-----+-----+-----+-----+-----+  
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 -----+-----+-----+-----+-----+-----+-----+  
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 1021 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA 1080  
 -----+-----+-----+-----+-----+-----+-----+  
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 -----+-----+-----+-----+-----+-----+-----+  
 AATTACACAATAATTACCCAATTAGATTAACCCCTTCCCTCTCTCCAACGTCTCACTCCA  
 1141 GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA 1200  
 -----+-----+-----+-----+-----+-----+-----+  
 CGTCTCGAACCACCTGCTACGGTTTTCTTATGACTTTGGAAATCACACAGGTGAGACCTT  
 1201 CTGCATCCAAATTCAGGTTCAAGTAATGATGTCATTATCCAAACATACCTTCTGTAAATTT 1260  
 -----+-----+-----+-----+-----+-----+-----+  
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 <---- 3.p53-BE ---->  
 1261 CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT 1320  
 -----+-----+-----+-----+-----+-----+-----+  
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 -----+-----+-----+-----+-----+-----+-----+  
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 1381 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAAATATAGCTGGGGCTATGCGATTTG 1440  
 -----+-----+-----+-----+-----+-----+-----+  
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 -----+-----+-----+-----+-----+-----+-----+  
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 -----+-----+-----+-----+-----+-----+-----+  
 GTCTCGGGATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCCTTG

TOCHID-1641660

GTCTGTGAGCCTCTCATGTTGCGAGCCACAACATGGACAGCCCAAGTCAAATGCCCCGCAAG  
1561 -----+-----+-----+-----+-----+-----+-----+ 1620  
CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCGGGTCAAGTTTACGGGGCGTTC  
  
TCTTTCTCTGAGTGAAGTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC  
1621 -----+-----+-----+-----+-----+-----+-----+ 1680  
AGAAAAGAGACTCACTGAGGTGCTTAATCGGTTCCGAGGACATGGGTCCGTCTGGAGACG  
  
GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCCAGGTTGAAGTACAGCAGAA  
1681 -----+-----+-----+-----+-----+-----+-----+ 1740  
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GCCCTTGAAGAAAGGCGAGGAGGCGGCTCTCGAGGTCTCACCTGAAGTGAGCATGCCAGC  
1741 -----+-----+-----+-----+-----+-----+-----+ 1800  
CGGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTTCG  
  
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1801 -----+-----+-----+-----+-----+-----+-----+ 1860  
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TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC  
1861 -----+-----+-----+-----+-----+-----+-----+ 1920  
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CCTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCTTCCCATCTCTCTGACCACCGGGGC  
1921 -----+-----+-----+-----+-----+-----+-----+ 1980  
GGAGGGGTTGGGCCCCGAAGGGGTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG  
  
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1981 -----+-----+-----+-----+-----+-----+-----+ 2040  
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2041 -----+-----+-----+-----+-----+-----+-----+ 2100  
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GCACGGAAACACACCCCTGAGGCCAGCCCTGGGTGCCCAGGCGGAGCTGCCTCTTCTCCCGC  
2101 -----+-----+-----+-----+-----+-----+-----+ 2160  
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GGACATGTACAGAGCTCGAGAAGTACTAGTGCCACGTGGGCGGTGCACCTTAAGCTTTA  
2161 -----+-----+-----+-----+-----+-----+-----+ 2220  
CCTGTACATGTCTCGAGCTCTTCATGATCACCAGGTGCACCGGCACGTGGAATTGAAAT  
  
----->  
  
GGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAGCCCTGAC  
2221 -----+-----+-----+-----+-----+-----+-----+ 2280  
CCCAGCGACCTCCCCCTGGGGCCAACTCTCTCCTCGCCTTGAGGACCTGTTCCGGGACTG  
  
----->  
  
AAGCCAAGCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGC  
2281 -----+-----+-----+-----+-----+-----+-----+ 2340  
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2341 -----+-----+-----+-----+-----+-----+-----+ 2400  
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2401 TAGGAAATAAGTCAACCCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT  
-----+-----+-----+-----+-----+-----+ 2460  
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2461 TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT  
-----+-----+-----+-----+-----+-----+ 2520  
AAAGAAAGAGCTTTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA  
  
2521 TTTTATTGTCACACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAA  
-----+-----+-----+-----+-----+-----+ 2580  
AAAATAACAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATT  
  
2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTCTGCCCCTTCTCTTTCT  
-----+-----+-----+-----+-----+-----+ 2640  
CTGACATTCAGCGACGGACTCACCAAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA  
  
2641 TCTTTTGGCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGG  
-----+-----+-----+-----+-----+-----+ 2700  
AGAAAACGGGAAAGAATCGAACGTGAGGGTACCACTAAAGACGAACCAGAGGACGACCCC  
  
2701 TTGGTGGTACTCGTTCCACCCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA  
-----+-----+-----+-----+-----+-----+ 2760  
AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACT  
  
2761 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG  
-----+-----+-----+-----+-----+-----+ 2820  
CGTCGGACAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTC  
  
2821 AGACGTG  
----- 2827  
TCTGCAC

T0240: T0240B00

Fig. 10

<---- 1.p53-BE ---->  
(promoter)

1 TGAGGACTCTCAGGAATATGCTGGTAAAATAAAAATAACCTTTAGAGATGCCCCAACTGT 60  
-----+-----+-----+-----+-----+  
ACTCCTGAGAGTCCTTATACGACCATTTTATTTTTATTGGAAATCTCTACGGGTTTGACA  
-->  
61 TTTCCCCAGAACACCAGCATTTCATTAGGTGTTTCATTCAATAGATTCTTCAAAGGATTCCA 120  
-----+-----+-----+-----+-----+  
AAAGGGGICTTGTGGTTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCCTAAGGT  
121 AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCCTTTGACATTAGCATAC 180  
-----+-----+-----+-----+-----+  
TTCCGTTTCTTCAAACCCCTTGTCTATATATTAATGGGTGGGAACTGTAATCGTATG  
181 TAAGGGCCCTGAGAAGTTTTGGATTAAAGAAAGTTTTCAAATTAAAGTAACCCAGAATTTT 240  
-----+-----+-----+-----+-----+  
ATTCCCGGGACTCTTCAAACCTAATTCTTTCAAAGTTTAATTTTCATTGGGTCTTAAAA  
241 CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT 300  
-----+-----+-----+-----+-----+  
GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA  
301 GAACCTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA 360  
-----+-----+-----+-----+-----+  
CTTGAACCTCTATTAATCTGCATGCACCCATCTCCCATCCCCTTCCCCCATACCGTATCT  
361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA 420  
-----+-----+-----+-----+-----+  
TTCTCGTCCTGGAACCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT

<---- 2.p53-BE ---->  
(promoter)

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTTATTTGTAAAG 480  
-----+-----+-----+-----+-----+  
TGATTGGTAGAAACGGTTACAACGAATTCGAAAAAACCGATGTAAAAAATAAACATTTT  
481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540  
-----+-----+-----+-----+-----+  
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCATAATTCATTCTCTAG  
541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT 600  
-----+-----+-----+-----+-----+  
GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA  
601 CCTTTCCCCTTTTTTCTCTCTTCCCTCCTTCATTCTCTTCCCTTACCTCTCCTTTC 660  
-----+-----+-----+-----+-----+  
GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGAATGGAGAGGAAAG  
661 CTTCCTCACACCCCTTTTCTCTCTTCCCTCCTTCATTCTCTTCCCTTACCTCTCCTTTC 720  
-----+-----+-----+-----+-----+  
GAAGGGAGTGTGGGAAAAGGAAGGAAGAAATGTAAAAAATAAATTTACTTGAAAAG  
721 ATTTTGAATAGTTTTAGGATTTCAAAAATTTGCAGAGATAATACAGAGAATGCCCAT 780  
-----+-----+-----+-----+-----+  
TAAACCTTATCMAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

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[illegible]

1741 CCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCTCACCTGAAGTGAGCATGCCAGCC 1800  
 -----+-----+-----+-----+-----+  
 GGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCGG  
 1801 ACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTGCAACGAACCTGACTCCTTCCT 1860  
 -----+-----+-----+-----+-----+  
 TGACGTCTTTCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGGA  
 1861 CACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC 1920  
 -----+-----+-----+-----+-----+  
 GTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGGTTCAACGACTTAGTTACCTCGG  
 1921 CTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCCTGACCACCGGGGCT 1980  
 -----+-----+-----+-----+-----+  
 GAGGGGTTGGGCCCCGAAGGGTCTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCGA  
 1981 TTTCTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC 2040  
 -----+-----+-----+-----+-----+  
 AAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCCACAAGTTTCTGCGAAG  
 2041 TGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGG 2100  
 -----+-----+-----+-----+-----+  
 ACCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCCGTGACC  
 2101 CACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCG 2160  
 -----+-----+-----+-----+-----+  
 GTGCCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCTCGACGGAGAAGAGGGCGC  
 2161 GGTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTCACTTCGGAGGATTGCTCA 2220  
 -----+-----+-----+-----+-----+  
 CCAACCACCTGGGCGAGTCATGCCTCAACCCCTTCGAGAAAGTGAAGCCTCCTAACGAGT  
 2221 ACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTGATCCCTCTCCTGCCCGGGTGG 2280  
 -----+-----+-----+-----+-----+  
 TGTGGTACGACCCGTAGACCTGGGAGGATGGAGACCCTAGGGAGAGGACGGGCCCCACC  
 2281 AGGCTTACCCGCTCTTAGTCCCGGGGATAGGCAAAGTGGGGCGGGCGCGGGACGCGTGCG 2340  
 -----+-----+-----+-----+-----+  
 TCCGAATGGGGCAGAATCAGGGCCCCCTATCCGTTTACCCCGCCCGCGCCCTGCGCACGC  
 2341 GGATTGCGGCGGCAGCGGCGCACGCGGGCACCTGGGAGCGGGCGGGCTGCTGCGGGAGGCG 2400  
 -----+-----+-----+-----+-----+  
 CCTAACGCCCGCGTCGCCGCGTGCGCCCGTGGACCCTCGCCGCCCCGACGACGCCCTCCGC  
 2401 TTGGAGACTGGCTCCCGGGGGCTGTTAGGACCTTCCTCAGGCCCGGGTGCTCAGAACGA 2460  
 -----+-----+-----+-----+-----+  
 AACCTCTGACCGAGGGCCCCCGACAATCCTGGAAGGGAGTCCGGGCCCCACGAGTCTTGCT  
 2461 TGGAGGACTTGCTTTTCTTGGGCTTGATGCGAAGTGCTGATCCCGCTGGGCAGGCGGGG 2520  
 -----+-----+-----+-----+-----+  
 ACCTCCTGAACGAAAAGAACCCGGAACCTACGCTTCACGACTAGGGCGACCCGTCCGCCCC  
 2521 CAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTTGAGGTGGGCGTGGGGGGCGGA 2580  
 -----+-----+-----+-----+-----+  
 GTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAACTCCACCCGCACCCCCGCT  
 2581 CAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCTGCTGGAGGGGGACCCCGGTTGGA 2640  
 -----+-----+-----+-----+-----+  
 GTCCTTAACCTTCGCCTTCAGACCCTTCGAAATCCAGCGACCTCCCCCTGGGGCCAACCT  
 2641 GAGAGGAGCGGAACCTCCTGGACAAGCCCTGACAAGCCAAAGGTCCGCTCCGGCGC 2700  
 -----+-----+-----+-----+-----+  
 CTCTCCTCGCCTTGAGGACCTGTTCCGGACTGTTCCGGTTCGGTTTCCAGGCGAGGCCGCG

<---- 4.p53-BE ---->  
 (intron)

GGGTGGGTGAGTGC GCGCCGCCCCGCGGGGCGGGGAGAGAGCCTACAGCCTTCAGAACA 2701  
-----+-----+-----+-----+-----+-----+ 2760  
CCCCCCCACTCACGCGCGGGGCGCCCCGCCCCCTCTCTCGGATGTCGGAAGTCTTGT  
CATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTG 2761  
-----+-----+-----+-----+-----+-----+ 2820  
GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTTATTTCAGTCGTGGCTTCGTCAC  
GTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTCTCGAAAAAGTTATATGGGGG 2821  
-----+-----+-----+-----+-----+-----+ 2880  
CAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAGAAAGAGCTTTTCAATATACCCCC  
CTGAATGAGCTTCTGGAGGCTTGTATACCGTTTTTTATTGTCACACAGAAAAGGAACTG 2881  
-----+-----+-----+-----+-----+-----+ 2940  
GACTTACTCGAAGACCTCCGAACAAATGGCAAAAAATAACAGTGTGTCTTTTCCTTTGAC  
CCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC 2941  
-----+-----+-----+-----+-----+-----+ 3000  
GGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACATTCAGCGACGGACTCACCAAAG  
ATTTTGTTTTGTCTTTCTGCCCTTCTCTTTCTTTTGGCCCTTTCTTAGCTTGCACTCC 3001  
-----+-----+-----+-----+-----+-----+ 3060  
TAAACAAAACAAAAGACGGGAAGAGAAAGAAAGAAACGGGAAGAATCGAACGTGAGG  
CATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCACCGCACAGA 3061  
-----+-----+-----+-----+-----+-----+ 3120  
GTACCACTAAAGACGAACCAGAGGACGACCCCAACCACCATGAGCAAGGGTGGCGTGTCT  
ACCCGGCGCCTATTATTGGGCAAGAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTC 3121  
-----+-----+-----+-----+-----+-----+ 3180  
TGGGCCGCGGATAATAACCGGTTCTTTGAACTCGTCGGACAAAACCTTTTCAGGGAGCGAG  
AGAAATGCCAGCTTGCAGATGGCTAATCAAAG 3181  
-----+-----+-----+-----+-----+-----+ 3212  
TCTTTACGGTCGAACGTCTACCGATTAGTTTC

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Fig 11

variations in the p53 binding region of figure 8

### 1. p1140 IMI

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMI GG**AAA**AGCCCTGACAAGCCA

↑

positions of the mutations (boldface and arrow): 2270 (C→A)

### 2. p1140 IMII

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMII GG**AAA**AGCCCTG**AAA**AGCCA

↑

↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2280 (C→A)

### 3. p1140 IMIII

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMIII GG**AAAT**CCCTG**AAAT**CCA

↑

↑

↑

↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2273 (G→T)

2280 (C→A)

2283 (G→T)

## 4. p1140 IMIV

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMIV GCACAAGCCCT**C**ACAAGCCA

↑

↑

positions of the mutations (boldface and arrow): 2268 (G→T)

2278 (C→A)

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Fig. 12

variations in the p53 binding regions of figure 9

### 1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GG <b>AAA</b> ATCCCTG <b>AAA</b> ATCCA
	↑    ↑            ↑    ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

### 2. p1141 1p53

p1141	AGAGATGCCCAAAGTGT
p1141 1p53	AGAGAT <b>T</b> CCCAA <b>A</b> ATGT
	↑                    ↑

positions of the mutations (boldface and arrow): 50

57

### 3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTT
p1141 2p53	AATGTT <b>T</b> CTTAAG <b>A</b> TTTT
	↑                    ↑

positions of the mutations (boldface and arrow): 443

450

## 4. p1141 3p53

p1141           AAACTACCTAAGAGCTATCT  
 p1141 3p53     **ACA**ATACCTAAGAGCTATCT  
                   ↑ ↑

positions of the mutations (boldface and arrow): 1268           (A→C)  
   1270           (C→A)

## 5. p1141 ΔBgl

p1141 3p53

                                  <---- 1.p53-BE ---->  
 p1141           AATAACCTTT**AGAGATG**CCCA**AACTG**TTTTCCCCAGAACA  
 p1141ΔBgl     AATAACCTTTA-----**GATCT**CCCCAGAACA

## 6. p1141 ΔSpe

p1141 3p53

                                  <---- 2.p53-BE ---->  
 p1141           CATCTTTGCC**AATGTTGCTTAAGCT**TTTTTTGGCTACATTT  
 p1141ΔBgl     CATCTTTGCCA-----**CTAGT**GGCTACATTT

## 7. p1141 ΔMph

                                  <---- 3.p53-BE ---->  
 p1141           AATTCATGCT**AACTACCTAAGAGCTATCT**ACCGTTCCAA  
 p1141ΔBgl     AATTCATGCT**ATGCA**-----**TACCGTTCCAA**

variations in the p53 binding region of figure 10

## 1. p1142 TAG

mutation of the positions: 2227 (A→T)  
2228 (T→A)

## 2. p1142 IMIII

p1142 GGACAAGCCCTGACAAGCCA  
p1142 IMIII GG**AA**ATCCCTGA**AA**ATCCA  
                  ↑   ↑           ↑   ↑

positions of the mutations (boldface and arrow): 2662 (C→A)  
2665 (G→T)  
2672 (C→A)  
2675 (G→T)

## 3. p1142 ΔBgl

<---- 1.p53-BE ---->  
p1142 AATAACCTTTAGAGATGCCCCAACTGTTTTCCCCAGAACA  
p1142ΔBgl AATAACCTTTA-----GATCTCCCCAGAACA

## 4. p1142 ΔSpe

<---- 2.p53-BE ---->  
p1142 CATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTT  
p1142ΔBgl CATCTTTGCCA-----CTAGTGGCTACATTT



## 5. p1142 ΔMph

&lt;---- 3.p53-BE ----&gt;

p1142

AATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA

p1142ΔBg1

AATTCATGCTATGCA-----TACCGTTCCAA

T02T40-T624E860

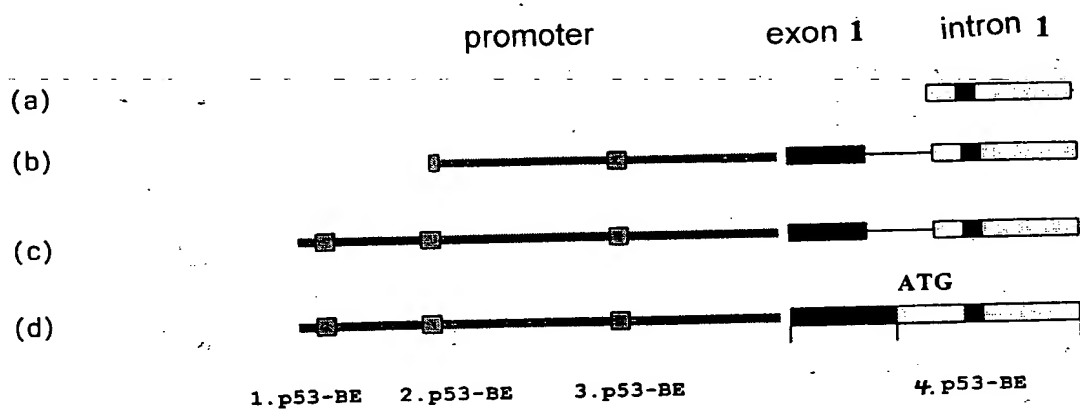


Fig. 14